REMARKS

Upon entry of the present amendment, claims 6, 8-10, and 31-37 will be pending in this application. Applicants have canceled claims 2, 14, 21-30, and 38-48 and amended claims 6 and 8-10. Support for the amendments can be found throughout the specification as filed. No new matter has been added. Claims 31, 34, and 35 are presently under consideration.

35 USC § 102

Claims 2, 21-23, 26, 28-30, 38, 39, 41, 43, 44, 46, and 48 were rejected as allegedly being anticipated by Davis et al. (WO 03/089624) or Davis et al. (US 7,317,087). Without conceding the rejection, applicants have canceled the above claims, solely to further prosecution. This moots the rejection.

35 USC § 103

Claims 2, 14, 21-24, 26, 28-31, 34-35, 38-39, 41, 43, 44, 46, and 48 were rejected as being allegedly unpatentable over Davis et al. (WO 03/089624) or Davis et al. (7,317,087), in view of Takao et al. (JP 2004-208583). Applicants have canceled claims 2, 14, 21-24, 26, 28-30, 38-39, 41, 43, 44, 46, and 48, without conceding the rejection with regard to those claims. Applicants traverse the rejection of claims 31, 34, and 35.

The invention is based, at least in part, on applicant's isolation from a natural killer cell line of a novel cDNA that encodes the polypeptide of SEQ ID NO:4. While not wishing to be bound by theory, applicants believe that the mRNA corresponding to the cDNA is one of multiple alternatively spliced mRNAs. Alternative splicing can allow a single genetic locus to produce multiple mRNAs, each of which can encode a different polypeptide or isoform. These protein isoforms can be differentially expressed in different cells or cell types. The existence of alternatively spliced versions can be difficult to predict.

Davis discloses a polypeptide having the sequence of SEQ ID NO:28, which is identical to residues 23-441 of claimed SEQ ID NO:4. Davis also discloses that SEQ ID NO:28 can be combined with a signal sequence of SEQ ID NO:32, which yields a polypeptide identical to residues 8-441 of SEQ ID NO:4.[1] The isolation of the cDNA encoding SEQ ID NO:32 and SEQ ID NO:28 from a human lymph node library is disclosed in Davis in Example 2. It appears that SEQ ID NO:40 describes the nucleic acid sequence of this cDNA. The sequence of SEQ ID NO:40 as disclosed by Davis differs from that of SEQ ID NO:3 of the instant application[2] in at least the 5' region of the nucleic acid.

Takao discloses a polypeptide having the sequence of SEQ ID NO:2, which is identical to residues 1-400 of claimed SEQ ID NO:4. This polypeptide was predicted from cDNA prepared from whole spleen. SEQ ID NO:2, as disclosed by Takao, also includes 13 additional amino acid residues at its carboxy terminus that differ from the carboxy-terminal 41 amino acids of claimed SEQ ID NO:4. Takao discloses the use of a computer program to predict the existence of a signal sequence at residues 1 or 2 to 24 of SEQ ID NO:2.

The Office action asserts that it would have been obvious to extend the signal sequence of Davis with the amino-terminal seven residues of the signal sequence of Takao. However, it is not clear that doing so would have been predicted to result in a functional signal sequence. Alternatively, if one were to simply replace the signal sequence of Davis with that of Takao, the resulting polypeptide sequence would contain a duplication of residues 23 and 24 relative to SEQ ID NO:4.

It is stated in the office action that it would have been obvious to combine Davis and Takao to reach the protein of the present invention. However, there is no indication of the rationale for selecting the polypeptides of Davis and Takao among numerous similar polypeptides. At the time of filing, various similar polypeptides likely to be additional splice variants were known, other than those of Davis and Takao. The polypeptides include:

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[1] At page 4, the Office action incorrectly states that "Davis teaches a polypeptide comprising SEQ ID NO: 32 (signal sequence) + SEQ ID NO: 28 (polypeptide sans signal sequence), which yields a polypeptide identical to residues ***6***-441 of claimed SEQ ID NO:4" (emphasis added). Later on the same page, the Office action correctly notes that "Davis does not teach the N-terminal 7 amino acids of SEQ ID NO:4."

[2] SEQ ID NO:3 is a nucleic acid that encodes the polypeptide of SEQ ID NO:4.

- SEQ ID NO:121 of WO 01/49728 (already of record), which describes a sequence identical to positions 70 to 441 of claimed SEQ ID NO:4 and also includes an amino-terminal 25-residue sequence not found in SEQ ID NO:4;

- SEQ ID NO:155 of WO 03/054152 (already of record), which describes a sequence identical to positions 6 to 364 of claimed SEQ ID NO:4 and also includes an amino-terminal 8-residue sequence not found in SEQ ID NO:4 and a carboxy-terminal 9-residue sequence not found in SEQ ID NO:4; and

- SEQ ID NO: 5 of EP 1201681 (already of record), which describes a sequence identical to positions 40 to 343 and 366 to 389 of claimed SEQ ID NO:4, with a deletion of residues 344 to 365 relative to SEQ ID NO:4, and also includes a carboxy-terminal 15-residue sequence not found in SEQ ID NO:4.

No reasoning is provided why one of skill in the art having knowledge of all of these disclosures would have been selected the polypeptides of Davis and Takao as starting points for modification. Additionally, no reasoning is provided why one of skill in the art having knowledge of the disclosures of Davis and Takao would have been motivated to modify the polypeptide of Davis with the residues of Takao to arrive at the claimed sequence. Rather, the Office appears to simply have used hindsight reasoning to derive the claimed polypeptides from vaguely related disclosures.

Additionally, even if one would have been motivated to combine the disclosures of Davis and Takao, it would not have been obvious that the result would have been a naturally occurring polypeptide. Polypeptides that occur naturally would have been predicted to be more biologically relevant than artificially produced polypeptides. The present specification describes the surprising identification of a naturally occurring mRNA encoding the polypeptide isoform of SEQ ID NO:4 (see Example 4). Further, the specification discloses that this particular isoform is present in natural killer cells, which are specialized immune cells thought to play a central role in innate immunity (see Background). The identification of SEQ ID NO:4, which is clearly distinct from the polypeptides disclosed in Davis and Takao, and its expression in natural killer cells provide a valuable contribution to the art of medicine.

In view of the above, claims 31, 34, and 35 would not have been obvious.

35 USC § 112, first paragraph

Claims 14, 21-24, 26, 28-30, 43, 44, 46, and 48 were rejected as allegedly failing to comply with the enablement and written description requirements. Without conceding the rejections, applicants have canceled the above claims, solely

to further prosecution. This moots the rejections.

CONCLUSION

Applicants respectfully submit that all claims are in condition for allowance, which action is requested. Applicants do not concede any positions of the Office that are not expressly addressed above, nor do applicants concede that there are not other good reasons for patentability of the presented claims or other claims.

This reply is being submitted with Petition for Extension of Time and the required fee. Please apply any other charges or credits to Deposit Account No. 06-1050, referencing Attorney Docket No. 14875-0157US1.

Respectfully submitted,

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